IN THE SPECIFICATION:

Page 1, please replace paragraph in the section headed: FIELD OF THE INVENTION with the following new paragraph:

--The present invention relates to a new[[,]] ~~microbiological~~[[,]] method for the production of α-L-aspartyl-L-phenylalanine (Asp-Phe) from the substrates L-aspartic acid (L-Asp) and L-phenylalanine (L-Phe). The present invention also relates to novel DNA fragments or combination of DNA fragments encoding a new Asp-Phe dipeptide synthetase, micro-organisms containing such DNA fragments, as well as to the new Asp-Phe dipeptide synthetases itself.--

Page 3, please replace the paragraph beginning on line 8, with the following new paragraph:

--Surprisingly, the inventors now found a new, and promising alternative ~~microbiological~~ method the production of α-L-aspartyl-L-phenylalanine (Asp-Phe) from the substrates L-aspartic acid (L-Asp) and L-phenylalanine (L-Phe) wherein the substrates are contacted, in the presence of an effective amount of adenosine-triphosphate (ATP), with a non-ribosomal dipeptide synthetase comprising two minimal modules connected by one condensation domain wherein the N-terminal module of these modules is recognising L-aspartic acid and the C-terminal module of these modules is recognising L-phenylalanine and is covalently bound at its N-terminal end to the condensation domain, and wherein each of these minimal modules is composed of an adenylation domain and a 4'-phosphopantetheinyl cofactor containing thiolation domain, and that the α-L-aspartyl-L-phenylalanine (Asp-Phe) formed is recovered.--

Page 9, please replace the Table 1, with the following new table including sequence ID numbers:

Domain	Core(s) Note: Former nomenclature is given in brackets	Consensus sequence
Adenylation	A1	L(TS)YxEL (SEQ ID NO:1)
	A2 (core 1)	LKAGxAYL(VL)P(LI)D (SEQ ID NO:2)
	A3 (core 2)	LAYxxYTSG(ST)TGxPKG (SEQ ID NO:3)
	A4	FDxS (SEQ ID NO:4)
	A5	NxYGPTE (SEQ ID NO:5)
	A6 (core 3)	GELxIxGxG(VL)ARGYL (SEQ ID NO:6)
	A7 (core 4)	Y(RK)TGDL (SEQ ID NO:7)
	A8 (core 5)	GRxDxQVKIRGxRIELGEIE (SEQ ID NO:8)
	A9	LpxYM(IV)P (SEQ ID NO:9)
	A10	NGK(VL)DR (SEQ ID NO:10)
Thiolation	T (core 6)	DxFFxxLGG(HD)S(LI) (SEQ ID NO:11)
Condensation	C1	SxAQxR(LM)(WY)XL (SEQ ID NO:12)
	C2	RHExLRTxF (SEQ ID NO:13)
	C3 (His)	MHHxISDG(WV)S (SEQ ID NO:14)
	C4	YxD(FY)AVW (SEQ ID NO:15)
	C5	(IV)GxFVNT(QL)(CA)xR (SEQ ID NO: 16)
	C6	(HN)QD(YV)PFE (SEQ ID NO:17)
	C7	RDxSRNPL (SEQ ID NO:18)
Thioesterase	TE	G(HY)SxG (SEQ ID NO:19)

Page 13, please delete the paragraph beginning on line12, and replace it with the following paragraph:

-- All known bacterial and some fungal peptide synthetase modules that incorporate the last amino acid into the growing peptide chain show a region with a thioesterase-like function. These regions of approximately 250 amino acids are located at the C-terminal end of the amino acid recognising modules. These thioesterase-like regions are integrated regions which exhibit homology to thioesterase-like proteins, and therefore also are referred to as the thioesterase domain ((integrated) TE-domain). All these integrated TE-domains contain an active site serine residue, which is part of the core motif GxSxG **(SEQ ID NO: 20** (see table 1). --

Page 21, immediately following the paragraph beginning on line 3, please add the following sentence:

--THIS SPACE IS INTENTIONALLY LEFT BLANK.--

Please delete the paragraph on page 31, beginning on line 17, and replace it with the following paragraph:

-- A 4934 bp fragment comprising regions from the *srf*B locus from chromosomal *Bacillus subtilis* ATCC 21332 DNA was amplified (PCR) using the following primers:
5' TAA GCA TGC TGC TTT CAT CTG CAG AAA C (5' *asp-leu-Sph*I- *srf*B2) **(SEQ ID NO:21)**, and
3' AAT GGA TCC TTC GGC ACG CTC TAC (3' *asp-leu-Bam*HI-*srf*B3) **(SEQ ID NO:22)**.--

Please delete the paragraph on page 32, beginning on line 20, and replace it with the following paragraph:

-- A 1894 bp chromosomal DNA-fragment from *Bacillus brevis* ATCC 8185 DNA was amplified (PCR) using the following primers:
5' ATT TGG TCA CCA ATC TCA TCG ACA A (5' *Bst*EII-TycA-NLID) **(SEQ ID NO:23)**,

and

5' ATA GGA TCC TGT ATT CGT AAA GTT TTT C (3'-PheAT-*Bam*HI) **(SEQ ID NO:24)**.

Please replace the paragraph on page 33, beginning at line 27, and replace it with the following new paragraph:

-- A 910 bp chromosomal DNA-fragment from *Bacillus subtilis* ATCC 21332 DNA was amplified (PCR) using the following primers:
5' ATA ATC GAT AAT CGC ACA AAT ATG GTC (5' TE-*srf*C1-*Cla*I) **(SEQ ID NO:25)** and
3' ATA AGA TCT AAC AAC CGT TAC GGT TTG TGT (3' int TE-*srf*C1-*Bgl*II) **(SEQ ID NO:26)**.--